

Applicant: Jay Short, et al.
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--42. (New) The method of claim 19, wherein each clone contains DNA obtained from a single organism.--

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--43. (New) The method of claim 19, wherein the library is a multispecies library.--

--44. (New) The method of claim 43, wherein the library is generated from a mixed population of uncultured organisms.--

--45. (New) The method of claim 43, wherein the library is generated from isolates.--

add E³
In The Specification

Applicants respectfully request entry of the following amendments:

On page 69, line 11, following the identified forward primer, please insert --(SEQ ID NO:1)--.
On page 69, line 13, following the identified reverse primer, please insert --(SEQ ID NO:2)--.

REMARKS

The present remarks are in response to the Office Action mailed December 7, 1999.

Claims 1-18 have been canceled without prejudice. New claims 19-45 have been added. Claims 1-18 were pending before this response. Original claim 18 was indicated to be "allowable if rewritten to overcome the rejection(s) under 35 USC 112, 2nd paragraph and to include all of the limitations of the base claim and any intervening claims (Office Action, page 13). By the present communication, claims 1-18 having been canceled and replaced with claims 19-45. These amendments add no new matter as the language of the new claims is fully supported by the specification and original claims.

The present invention provides methods for identifying a bioactivity or biomolecule of interest using high throughput screening of DNA by screening a library containing a plurality of clones obtained from more than one organism. Preferably, each clone contains DNA obtained